



1	CGGTGGCGCCGTTCTAGAACTAGTGGATCCCCGGGATGCAGGAATTGGCACGAGAAA	60
61	GTGCGGCGAAAGTAAGAGGCTCACTGGGAAGACTGCCGGGATCCAGGTCTCCGGGGTC	120
121	CGCTTGCCAGAGGCAGGAAGCAGTGCCGGCAGACACTGCACCCATCCGGCTG	180
181	CTTTGCTGCCCTCTCAGCTCCAAAGAAAGGCATCGTCATGTGATCATCACCTAAGA	240
241	ACTAGAACATCAGCAGGCCCTAGAACGCCTCACTCTGCCCTCCCTTAATATCTCAA	300
301	GGATGACACTTCTGGGTGTAGTGAATCTACTTTATGGAATCCTGCAAAGTGATG	360
	M T L L W C V V S L Y F Y G I L O S D A	
361	CCTCAGAACGCTCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTGAAG	420
	S E R C D D W G L D T M R Q I Q V F E D	
421	ATGAGCCAGCTCGCATCAAGTGCCCCTCTGAACACTTCTGAAATTCAACTACAGCA	480
	E P A R I K C P L F E H F L K F N Y S T	
481	CAGCCCATTAGCTGCCCTACTCTGATCTGGTATTGGACTAACGAGGACCGGGACCTTG	540
	A H S A G L T L I W Y W T K Q D R D L E	
541	AGGAGCCAATTAACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGT	600
	E P I N F R L P E N R I S K E K D V L W	
601	GGTTCCGGCCCCTCTCCTCAATGACACTGGCAACTATACTGCATGTTAAGGAACACTA	660
	F R P T L L N D T G N Y T C M L R N T T	
661	CATATTGCAGCAAAGTTGCATTTCCCTGGAAAGTTGTTAAAAAGACAGCTGTTCAATT	720
	Y C S K V A F P L E V V Q K D S C F N S	
721	CCCCCATGAAACTCCAGTGCATAAACTGTATAGAATATGGCATTAGGAGATCACTT	780
	P M K L P V H K L Y I E Y G I Q R I T C	
781	GTCCAAATGTAGATGGATATTTCTCCAGTGTCAAACCGACTATCACTGGTATATGG	840
	P N V D G Y F P S S V K P T I T W Y M G	
841	GCTGTTATAAAATACAGAATTAAATAATGTAATACCCGAAGGTATGAACCTTGAGTTCC	900
	C Y K I Q N F N N V I P E G M N L S F L	
901	TCATTGCCCTAATTCAAATAATGGAAATTACACATGTGTTGTTACATATCCAGAAAATG	960
	I A L I S N N G N Y T C V V T Y P E N G	
961	GACGTACGTTCATCTCACCAAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAATG	1020
	R T F H L T R T L T V K V V G S P K N A	
1021	CAGTCCCCCTGTGATCCATTACCTTAATGATCATGTGGTCTATGAGAAAGAACAGGAG	1080
	V P P V I H S P N D H V V Y E K E P G E	
1081	AGGAGCTACTCATTCCGTACGGCTATTAGTTCTGATGGATTCTCGCAATGAGG	1140
	E L L I P C T V Y F S F L M D S R N E V	
1141	TTGGTGGACCATTGATGGAAAAAAACCTGATGACATCACTATTGATGTCACCATTAAAG	1200
	W W T I D G K K P D D I T I D V T I N E	
1201	AAAGTATAAGTCATAGTAGAACAGAAGATGAAACTAGAACATGAGATTTGAGCATCAAGA	1260
	S I S H S R T E D E T R T Q I L S I K K	
1261	AAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCCAAAGGCG	1320
	V T S E D L K R S Y V C H A R S A K G E	
1321	AAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAGGTAAAGATGCGGTAGTGATGAATCT	1380
	V A K A A K V K Q K G N R C G Q *	

2/5

1381	CTCAGCTCAAATTAAACATTGGTGGTGAATAAGGACAAAAGGAGAGATTGAGAACAGAGA	1440
1441	GCTCCAGCACCTAGCCTGACGGCATCTAACCCATAGTAATGAATCAAACCTAAATGAAAAA	1500
1501	ATATGAAAGTTTCATCTATGTAAGATACTCAAAATATTGTTCTGATATTGTTAGTACC	1560
1561	GTAATGCCCAAATGTAGCTAAAAAAATCGACGTGAGTACAGTGAGACACAATTGTGTC	1620
1621	TGTACAATTATGAAAAATTAAAAACAAAGAAAATATTCAAAGCTACCAAAGATAGAAAAA	1680
1681	ACTGGTAGAGCCACATATTGGTGGTGAATTATTAAGACCCTTTAAAAATCATTGTTG	1740
1741	AGAGTTAACAGAGTCATAAAAAGATTGCATCATCTGACCTAACAGACTTCGGAATTTC	1800
1801	TGAACAAATAACAGAAAAGGAAATTATACCTTTAATATTAGAACGATTATCTGTA	1860
1861	GTTGTAACATTAAATAGCAGCCATCCAATTGTATGCAACTATTAAAGGTATTGAAT	1920
1921	GTTTATTTCCAAAATGCATAATTATAATTATTAAACACTATGTATCAATATT	1980
1981	AGCAGGTTATAATATACCAGCAGCCACAATTGCTAAAATGAAAATCATTAAATTATGA	2040
2041	TTTAAATGGTATACACATGATTCTATGTTGATAGTACTATATTCTACAATAAATG	2100
2101	GAAATTATAAAGCCTCTTGTCAAGTGTGCTCCTAAAAAAAAAAAAAAA	2155

FIG. 1B

3/5

Query: 303 MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYST 482
M LLW ++SL FYGILQS ASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLK+NYST
Sbjct: 1 MGLLWYLMSSLFYGILQSHASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYST 60

Query: 483 AHSAGLTTLIWWYWTQKDRDLEPINFRLPENRISKEKDVLWFRPTLNDTGNYTCMLRNTT 662
AHS+GL TLIWYWT+QKDRDLEPINFRLPENRISKEKDVLWFRPTLNDTGNYTCMLRNTT
Sbjct: 61 AHSSGLTTLIWWTRQKDRDLEPINFRLPENRISKEKDVLWFRPTLNDTGNYTCMLRNTT 120

Query: 663 YCSKVAFPLEVVQKDCSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMG 842
YCSKVAFPLEVVQKDCSCFNS M+ PVHK+YIE+GI +ITCPNVDGYFPSSVKP++TWY G
Sbjct: 121 YCSKVAFPLEVVQKDCSCFNSAMRFPVHKMYIEHGIHKITCPNVDGYFPSSVKPSVTWYKG 180

Query: 843 CYKIQNNVVIPEGMNLSQLIALISMNIGNYTCVVTPENGRTFHLLTRTLTVKVVGSPKNA 1022
C +I +F+NV+PEGMNL SF I L+SNMIGNYTCVVTPENGRI FHL TRT+TVKVVGSPK+A
Sbjct: 181 CTEIVDFHNVLPEGMNLSQLFPIVSVNIGNYTCVVTPENGRLFHL TRTVTVKVVGSPKDA 240

Query: 1023 VPPVJHSPNDHVYYKEPGEELLIPCTVYFSFLMSRNEWMWTIDGKPKDDITIDVTINE 1202
+PP I+SPND VVYEKEPGEEL+IPC VYFSF+MDS NEWWWMTIDGKPKDD+T+D+TINE
Sbjct: 241 LPPQIYSPNDRVYYKEPGEELVIPCKVYFSFIMDSHNEWWWMTIDGKPKDDVTVDITINE 300

Query: 1203 SISHSRTEDETRTQILSIKKVTSDELKRSYVCHARSAKGEVAKAKVKQK 1352
S+S+S TEDETRTQILSIKKV EDL+R+YVCHAR+ KGE +AAKVKQK
Sbjct: 301 SVSYSSTTEDTRTQILSIKKVTPEDLRRNYVCHARNTKGEAEQAAKVKQK 350

FIG. 2A

4/5

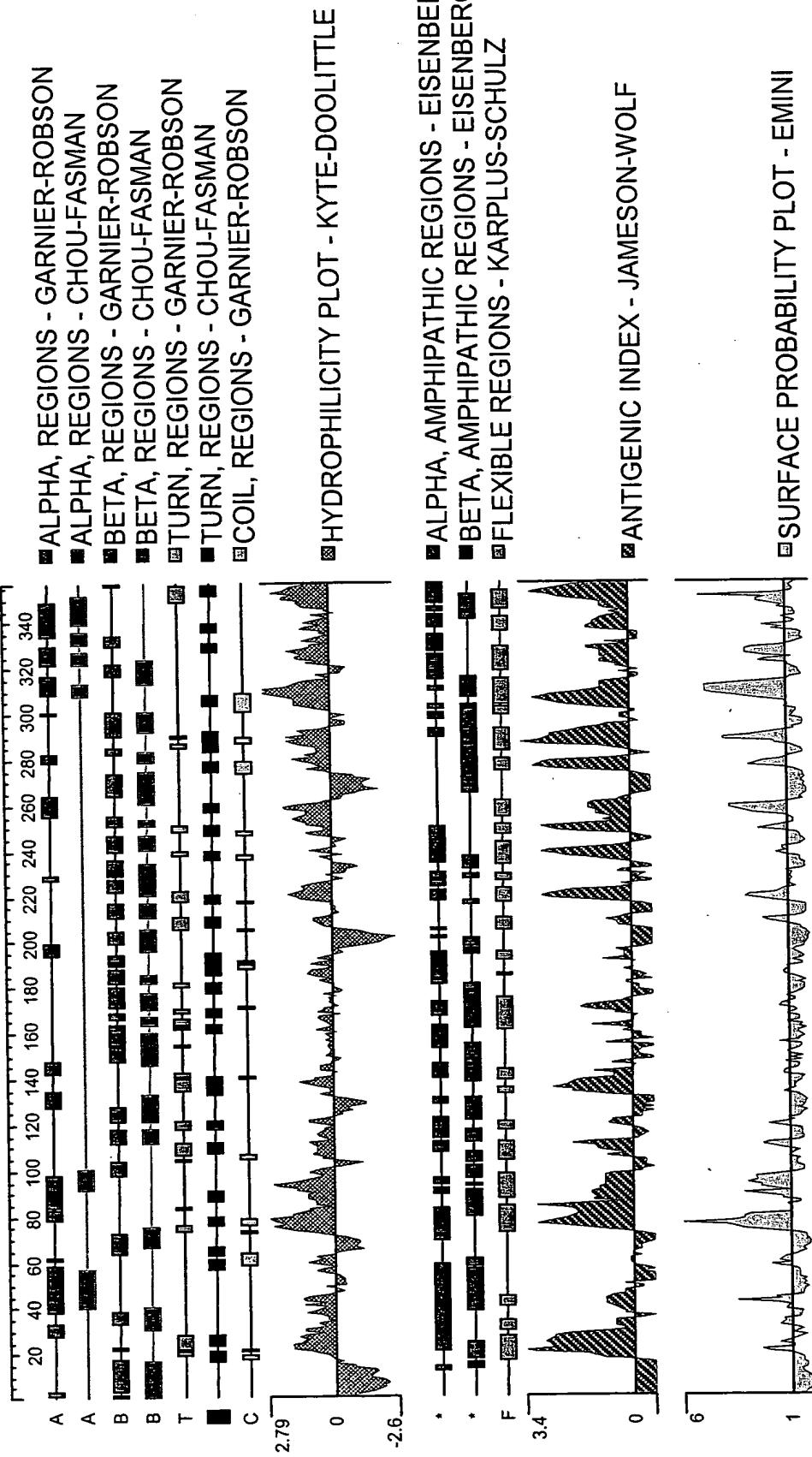
1 TCTATGAGAAAGAACCAAGGAGAGGAGCTACTCATTCCCTGTACGGTCTAT 50
|||||
1060 TCTATGAGAAAGAACCAAGGAGAGGAGCTACTCATTCCCTGTACGGTCTAT 1109
|||||
51 TTTAGTTTCTGATGGATTCTCGCAATGAGGTTGGTGGACCATTGATGG 100
|||||
1110 TTTAGTTTCTGATGGATTCTCGCAATGAGGTTGGTGGACCATTGATGG 1159
|||||
101 AAAAAAACCTGATGACATCACTATTGATGTCACCATTAAACGAAAGTATAA 150
|||||
1160 AAAAAAACCTGATGACATCACTATTGATGTCACCATTAAACGAAAGTATAA 1209
|||||
151 GTCATAGTAGAACAGAACAGATGAAACAAGAACACTCAGATTTGAGCATCAAG 200
|||||
1210 GTCATAGTAGAACAGAACAGATGAAACAAGAACACTCAGATTTGAGCATCAAG 1259
|||||
201 AAAGTTACCTCTGAGGATCTCAAGCGCANTANTGTCTGTATGCTAGAACG 250
|||||:
1260 AAAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTATGCTAGAACG 1259
|||||
251 TGCCAAAGGCGAAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAG 294
|||||
1310 TGCCAAAGGCGAAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAG 1353

FIG.2B

FIG. 3 REPLACEMENT SHEET

Applicant: Bednarik, et al.
 Application No.: 08/917,710
 Title: Soluble Interleukin-1 Receptor Accessory Molecule

5/5



MTLLWCVVS_LFYGILQSDASERCDDWGLDTMRQIQQVFEDEPARIKCPLFEHFLKFNYSTAHSAGLTLIWYWTKQDRDLEEINFRPENRISKEKDV
 LWFRPTLLNDTGNYTCMLRNTTYCSKVAFFPLVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNYDGYFPSSVKPTWYMGCYKIQNFNNVPEGMIN
 LSFLALISNNGNYTCVVTYPENGRTFHLTRTLTVKVGSPKNAVPVISPNDHVVYKEPGEELLLPCTVFSFLMDSRNEVWWTIDGKPDDDITD
 TINESISHSRTDETRTQILSIKKVTSEDLKRSYVCHARSAAKGEVAKVKQKGNRCGQ.

FIG. 3